FIGURE 1

```
SP22   1   MASKRALVILAKGAEEMETVIPVDIMRRAGIKVTVAGLAGKDPVQCSRDV  50
           |||||||||||||||||||||||||||:||||||||||||||||||||||
DJ-1   1   MASKRALVILAKGAEEMETVIPVDVMRRAGIKVTVAGLAGKDPVQCSRDV  50
                                                Peptide 1

SP22   51  VICPDTSLEEAKTQGPYDVVVLPGGNLGAQNLSESALVKEILKEQENRKG  100
           |||||.|||:||  ||||||||||||||||||||||:|||||||||||||
DJ-1   51  VICPDASLEDAKKEGPYDVVVLPGGNLGAQNLSESAAVKEILKEQENRKG  100
                                                Peptide 2

SP22   101 LIAAICAGPTALLAHEVGFGCKVTSHPLAKDKMMNGSHYSYSESRVEKD  149
           ||||||||||||||||:| |:|||:||||||||||| ||:||| |||||
DJ-1   101 LIAAICAGPTALLAHEIGCGSKVTTHPLAKDKMMNGGHYTYSENRVEKD  149
                                   Peptide 3

SP22   150 GLILTSRGPGTSFEFALAIVEALSGKDMANQVKAPLVLKD  189
           ||||||||||||||||||||||| ||::| ||||||||||
DJ-1   150 GLILTSRGPGTSFEFALAIVEALNGKEVAAQVKAPLVLKD  189
           Peptide 4
```

FIGURE 2

```
1   A gctgtgcagagccgtctggcagggttgacctcctaaagggatattccatctttattaatcattag 65

66  A tagtgtggtcagagacttagcaccattggtctcccccaacctggtccagacatttcagcagttta 130

131 A tcggaacagcaacaacagcaacaaaaccttcaaaatttacaagtctttaagaaatagaaATGgca 195
    B         tggcttcgcgtgggtggaggaggcgcggctgcaggtctttaagaaatagaaATGgca

1                                                                 M  A  2

196   tccaaaagagctctggtcatcctagccaaaggagcagaggagatggagacagtgattcctgtgga 260
16     S  K  R  A  L  V  I  L  A  K  G  A  E  E  M  E  T  V  I  P  V  D 24

261   catcatgcggcgagctgggattaaagtcaccgttgcaggcttggctgggaaggaccccgtgcagt 325
38     I  M  R  R  A  G  I  K  V  T  V  A  G  L  A  G  K  D  P  V  Q   45
                                Peptide 1

326   gtagccgtgatgtagtgatttgtccggataccagtctggaagaagcaaaaacacagggaccatac 390
59    C  S  R  D  V  V  I  C  P  D  T  S  L  E  E  A  K  T  Q  G  P  Y  67

391   gatgtggttgttcttccaggaggaaatctgggtgcacagaacttatctgagtcggctttggtgaa 455
81     D  V  V  V  L  P  G  G  N  L  G  A  Q  N  L  S  E  S  A  L  V  K 89

456   ggagatcctcaaggagcaggagaacaggaagggcctcatagctgccatctgtgcgggtcctacgg 520
103    E  I  L  K  E  Q  E  N  R  K  G  L  I  A  A  I  C  A  G  P  T   110
        Peptide 2
                                          *
521   ccctgctggctcacgaagtaggctttggatgcaaggttacatcgcacccattggctaaggacaaa 585
124   A  L  L  A  H  E  V  G  F  G  C  K  V  T  S  H  P  L  A  K  D  K  132
                                          Peptide 3

586   atgatgaacggcagtcactacagctactcagagagccgtgtggagaaggacggcctcatcctcac 650
146    M  M  N  G  S  H  Y  S  Y  S  E  S  R  V  E  K  D  G  L  I  L  T 154
                                                      Peptide 4

651   cagccgtgggcctgggaccagcttcgagtttgcgctggccattgtggaggcactcagtggcaagg 715
168    S  R  G  P  G  T  S  F  E  F  A  L  A  I  V  E  A  L  S  G  K   175

716   acatggctaaccaagtgaaggccccgcttgttctcaaagacTAGagagcccaagccctggaccct 780
189   D  M  A  N  Q  V  K  A  P  L  V  L  K  D  *                     189

781   ggacccccaggctgagcaggcattggaagcccactagtgtgtccacagcccagtgaacctggcat 845

846   tggaagcccactagtgtgtccacagcccagtgaacctcaggaactaacgtgtgaagtagcccgct 910

911   gctcaggaatctcgccctggctctgtactattctgagccttgctagtagaataaacagttcccca 975

976   agctc*c*tgacggct*                                                 985
```

Figure 3

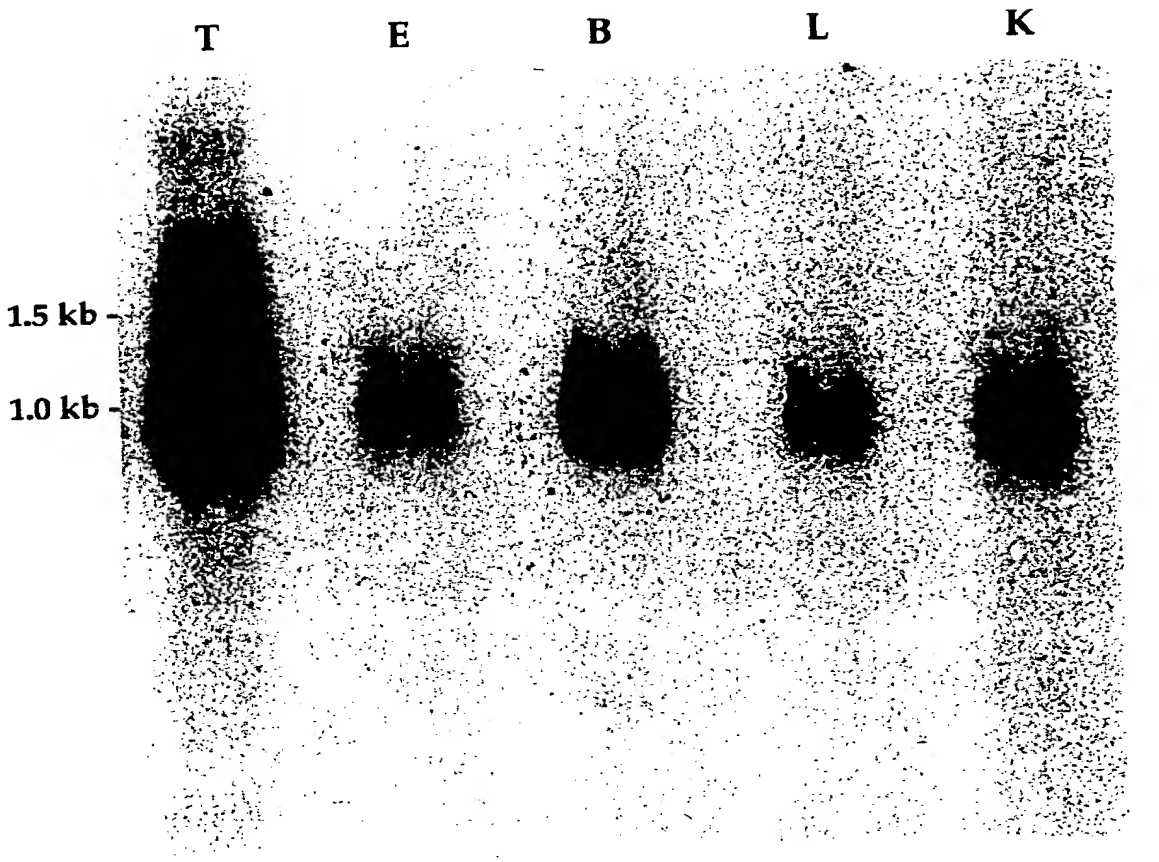


Figure 4

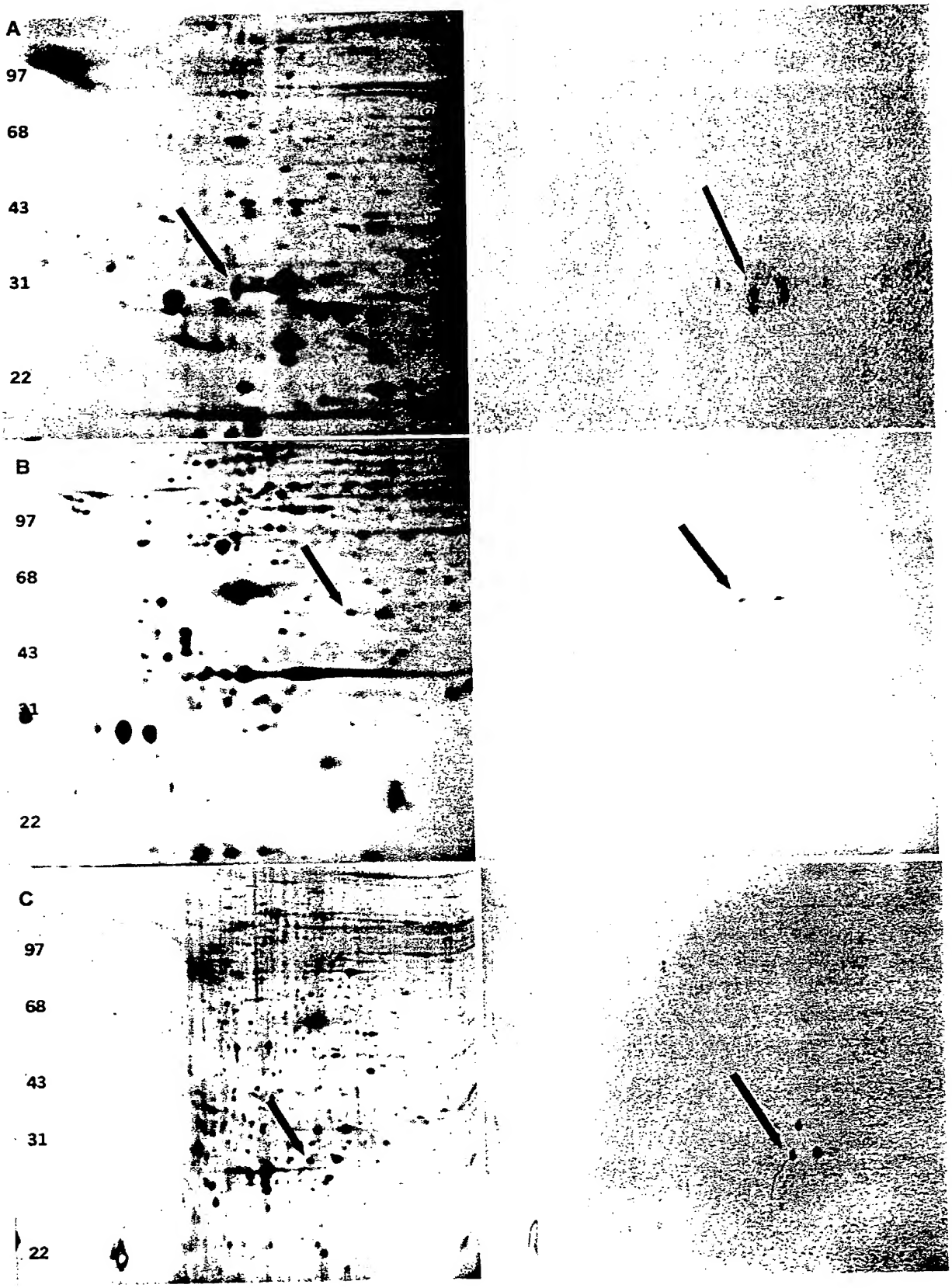


Figure 5

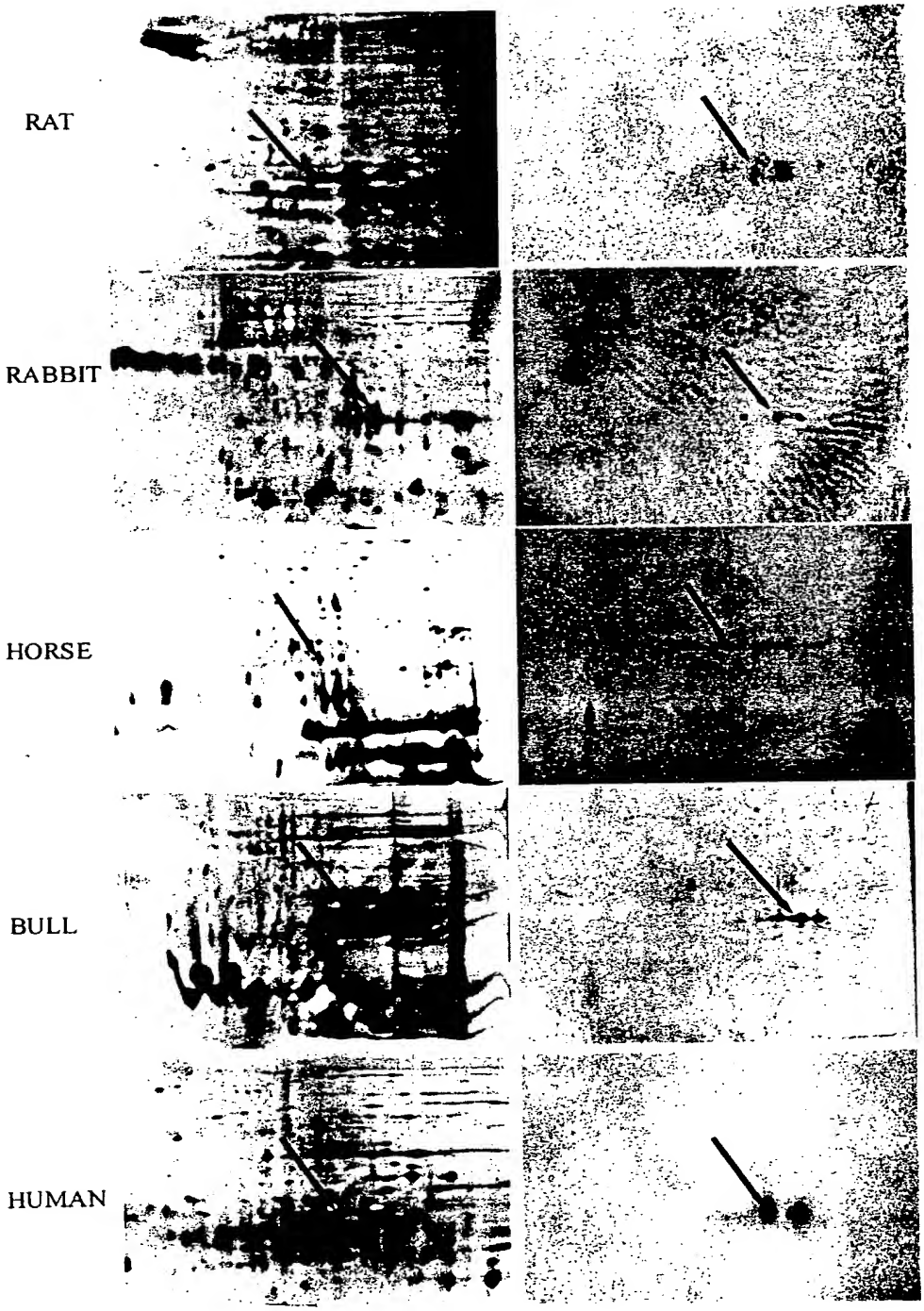
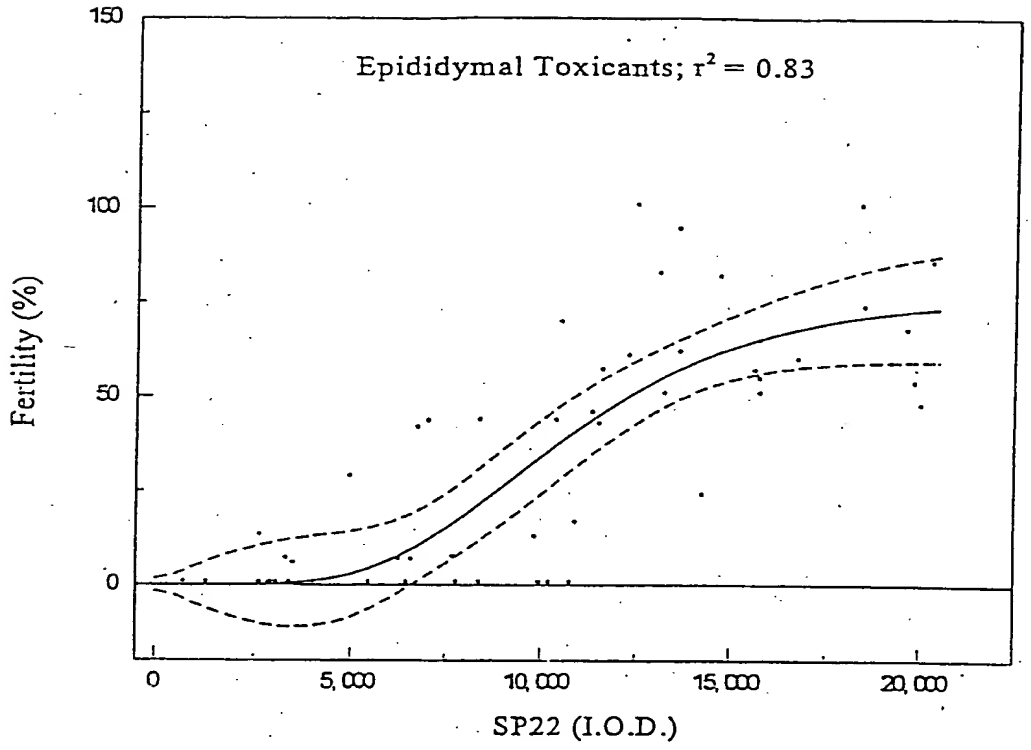


Figure 6



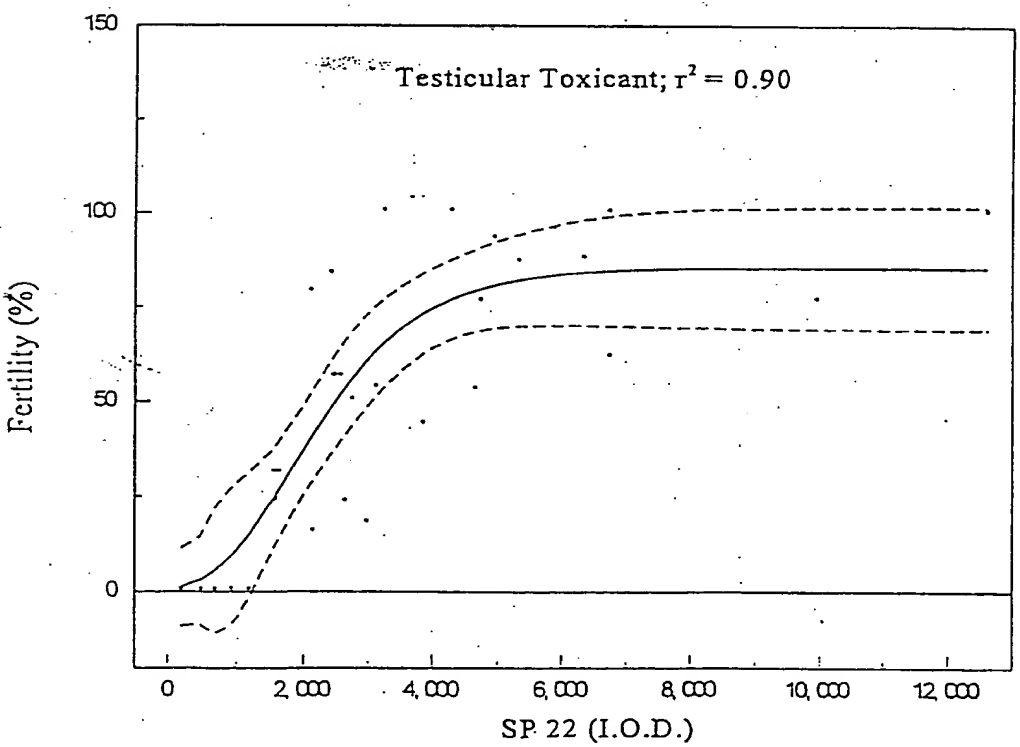


Figure 7

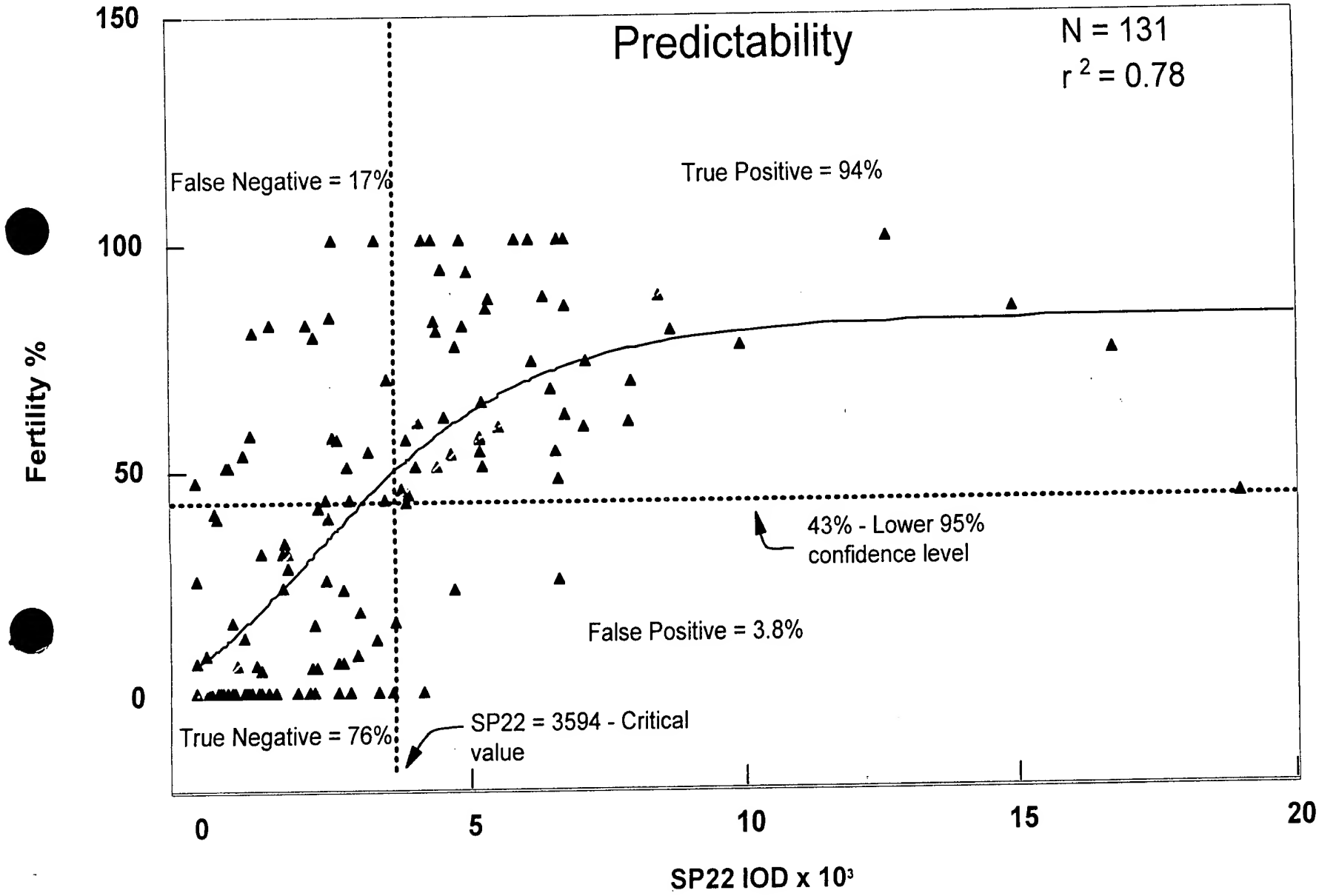


Figure 8

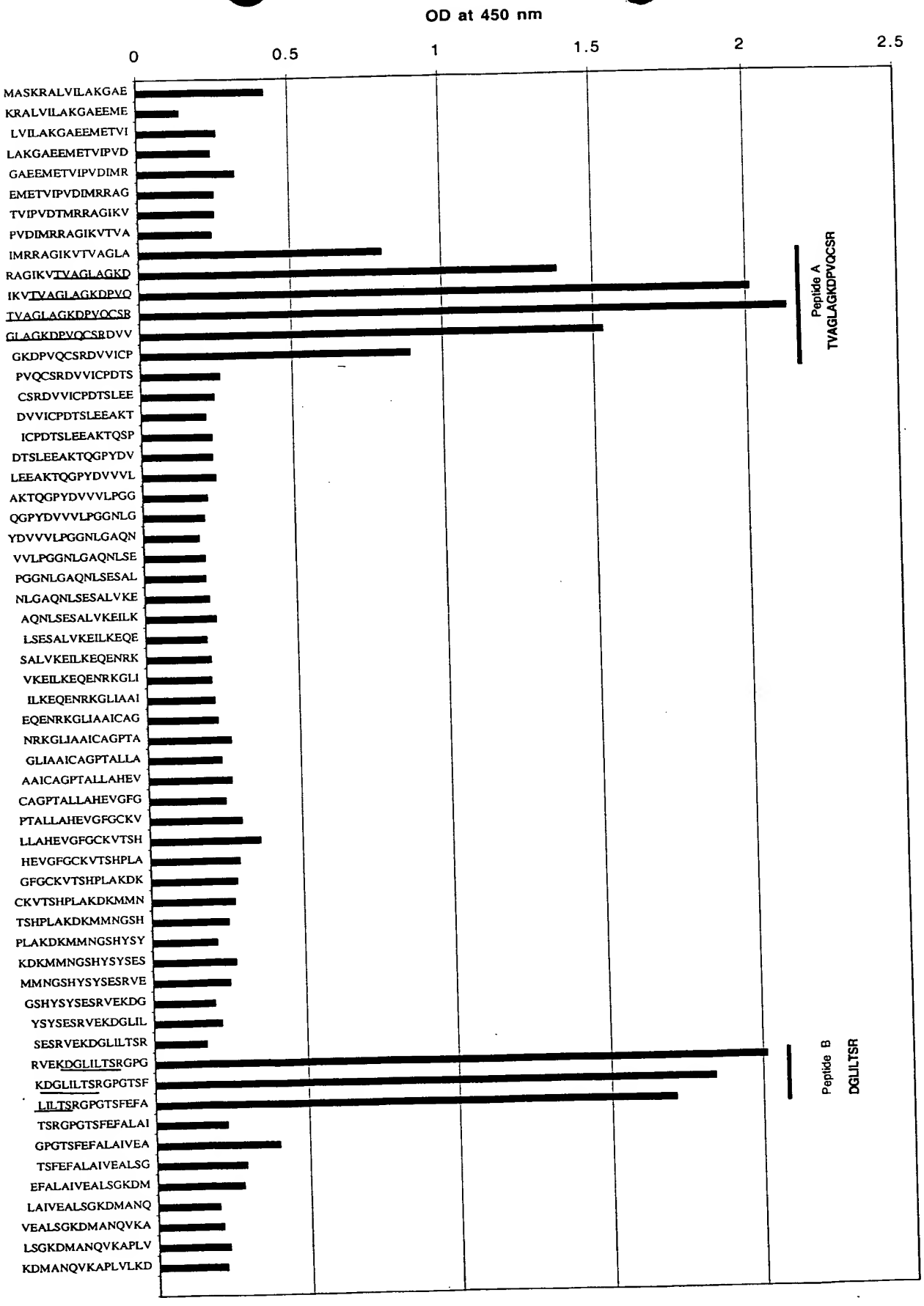

OD at 450 nm
0
0.5
1
1.5
2
2.5
Sequential Sp22 15 MER Peptides
MASKRALVILAKGAE
KRALVILAKGAEEME
LVILAKGAEEMETVI
LAKGAEEMETVIPVD
GAEEMETVIPVDIMR
EMETVIPVDIMRRAG
TVIPVDTMRRAGIKV
PVDIMRRAGIKVTVA
IMRRAGIKVTVAGLA
RAGIKVTVAGLAGKD
IKVTVAGLAGKDPVQ
TVAGLAGKDPVQCSR
GLAGKDPVQCSRDVV
GKDPVQCSRDVVICP
PVQCSRDVVICPDTS
CSRDVVICPDTSLEE
DVVICPDTSLEEAKT
ICPDTSLEEAKTQSP
DTSLEEAKTQGPYDV
LEEAKTQGPYDVVVL
AKTQGPYDVVVLPGG
QGPYDVVVLPGGNLG
YDVVVLPGGNLGAQN
VVLPGGNLGAQNLSE
PGGNLGAQNLSESAL
NLGAQNLSESALVKE
AQNLSESALVKEILK
LSESALVKEILKEQE
SALVKEILKEQENRK
VKEILKEQENRKGLI
ILKEQENRKGLIAAI
EQENRKGLIAAICAG
NRKGLIAAICAGPTA
GLIAAICAGPTALLA
AAICAGPTALLAHEV
CAGPTALLAHEVGFG
PTALLAHEVGFGCKV
LLAHEVGFGCKVTSH
HEVGFGCKVTSHPLA
GFGCKVTSHPLAKDK
CKVTSHPLAKDKMMN
TSHPLAKDKMMNGSH
PLAKDKMMNGSHYSY
KDKMMNGSHYSYSES
MMNGSHYSYSESRVE
GSHYSYSESRVEKDG
YSYSESRVEKDGLIL
SESRVEKDGLILTSR
RVEKDGLILTSRGPG
KDGLILTSRGPGTSF
LILTSRGPGTSFEFA
TSRGPGTSFEFALAI
GPGTSFEFALAIVEA
TSFEFALAIVEALSG
EFALAIVEALSGKDM
LAIVEALSGKDMANQ
VEALSGKDMANQVKA
LSGKDMANQVKAPLV
KDMANQVKAPLVLKD
Peptide A
TVAGLAGKDPVQCSR
Peptide B
DGLILTSR

Figure 9

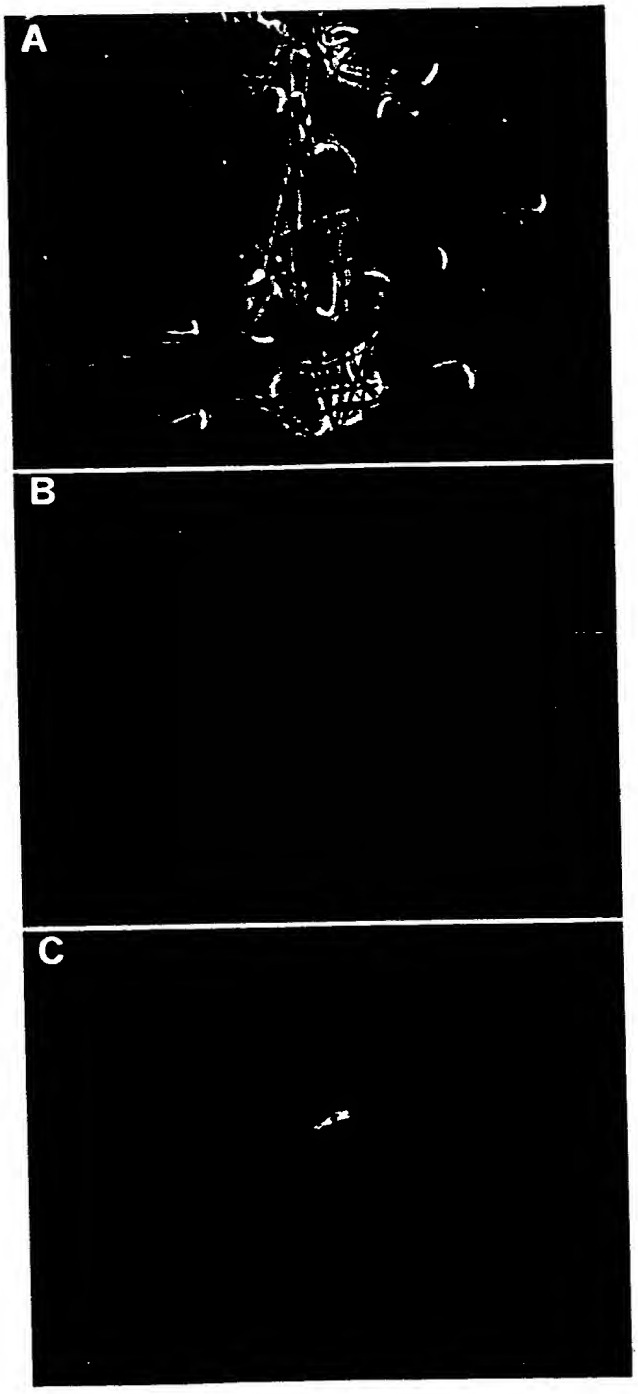


Figure 10

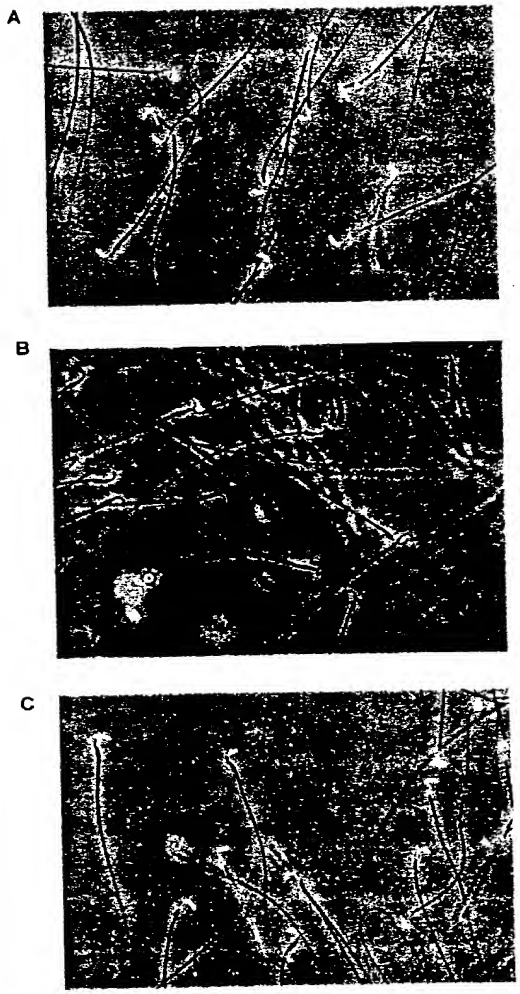


Figure 11

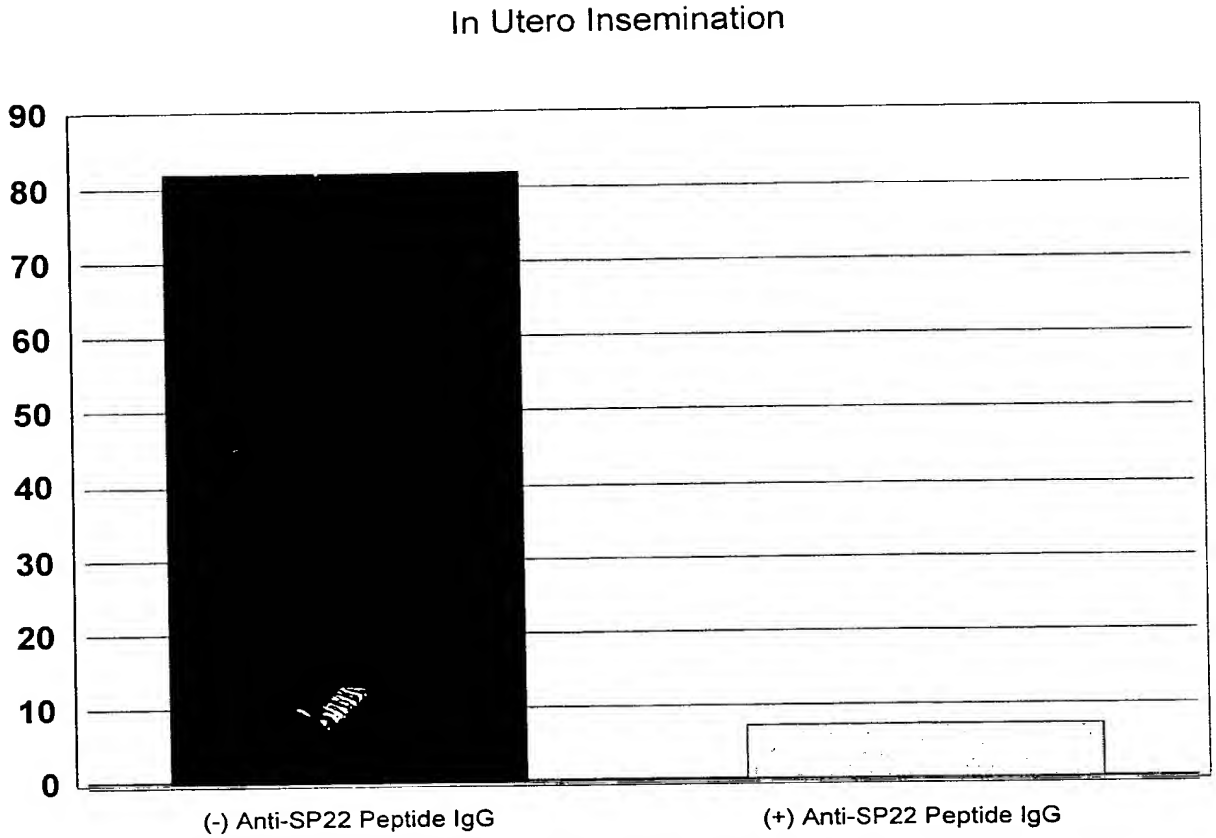

In Utero Insemination
Fertility (Implants / Corpora Lutea)
90
80
70
60
50
40
30
20
10
0
(-) Anti-SP22 Peptide IgG
(+) Anti-SP22 Peptide IgG

Figure 12

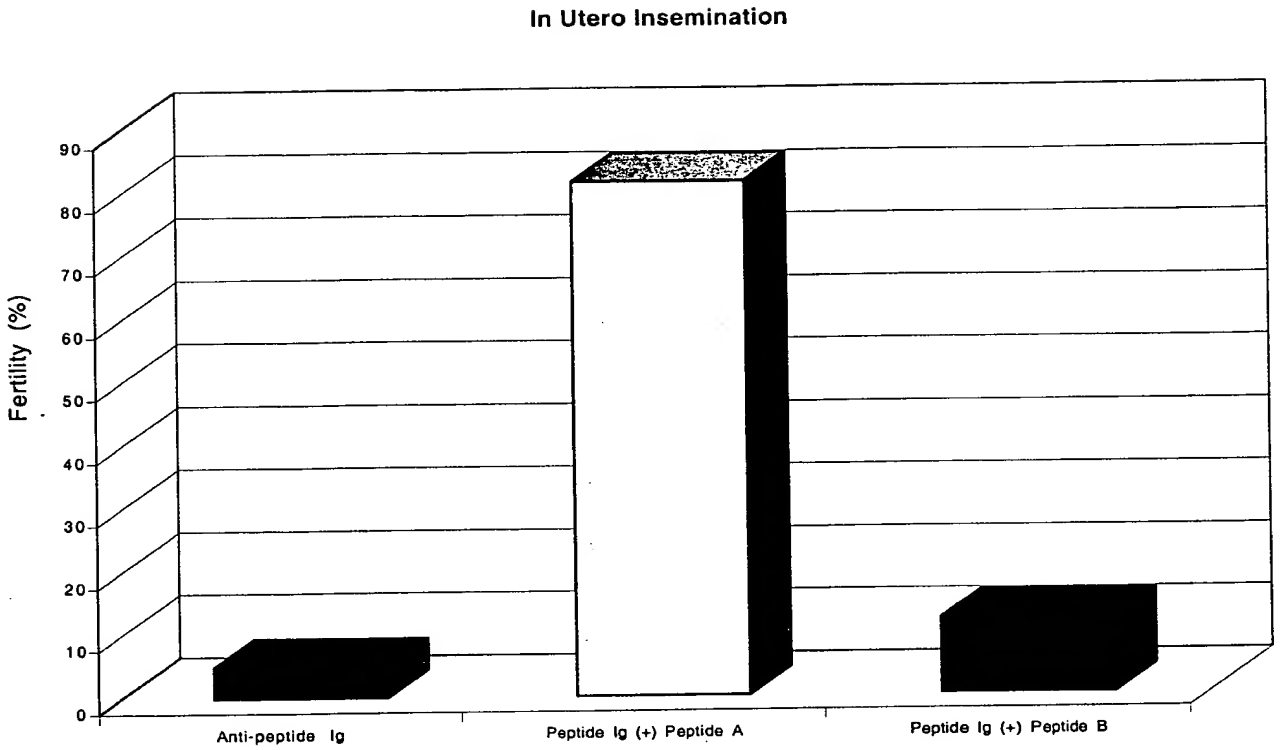

In Utero Insemination
Fertility (%)
90
80
70
60
50
40
30
20
10
0
Anti-peptide Ig
Peptide Ig (+) Peptide A
Peptide Ig (+) Peptide B

Figure 13

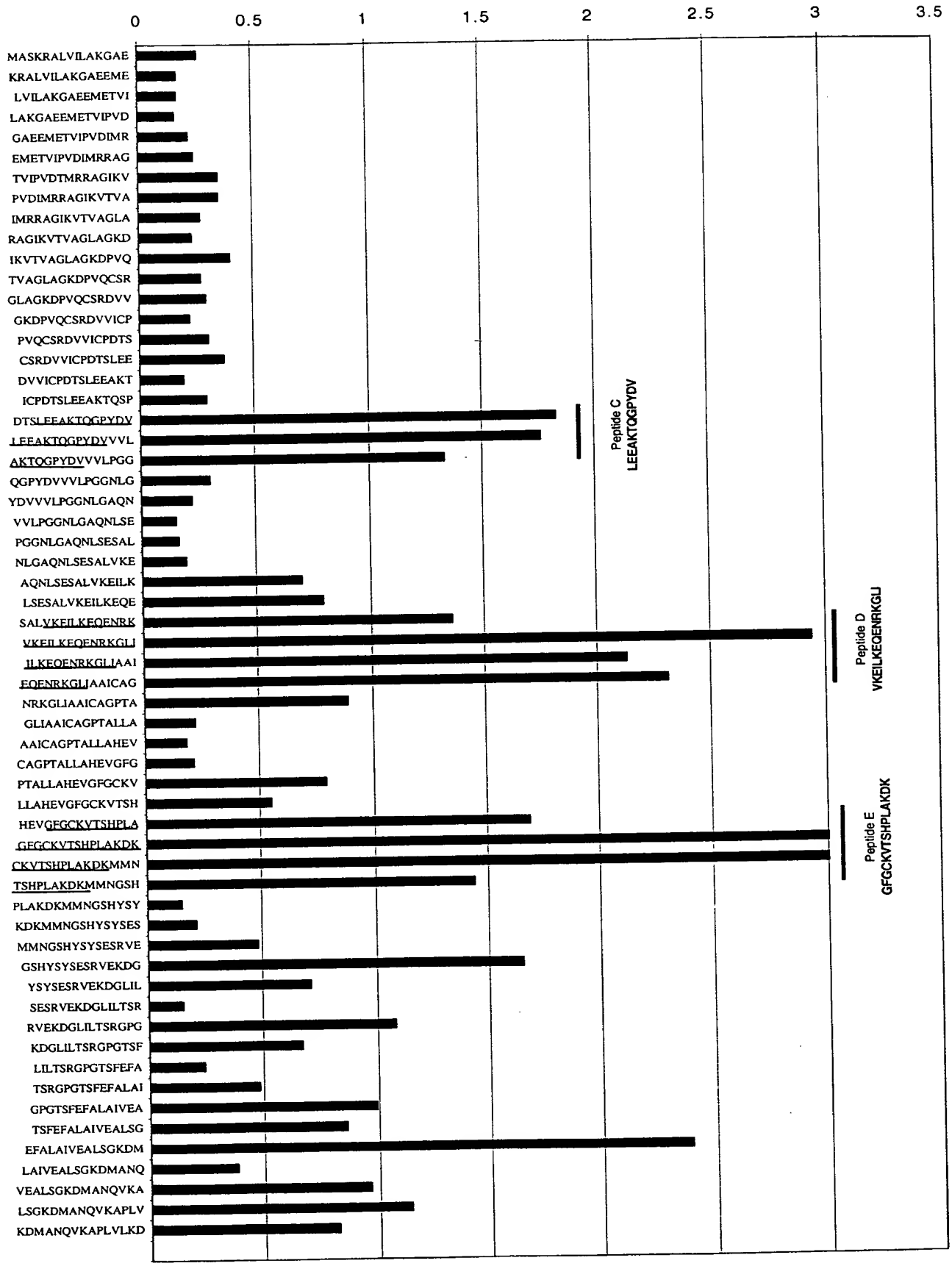
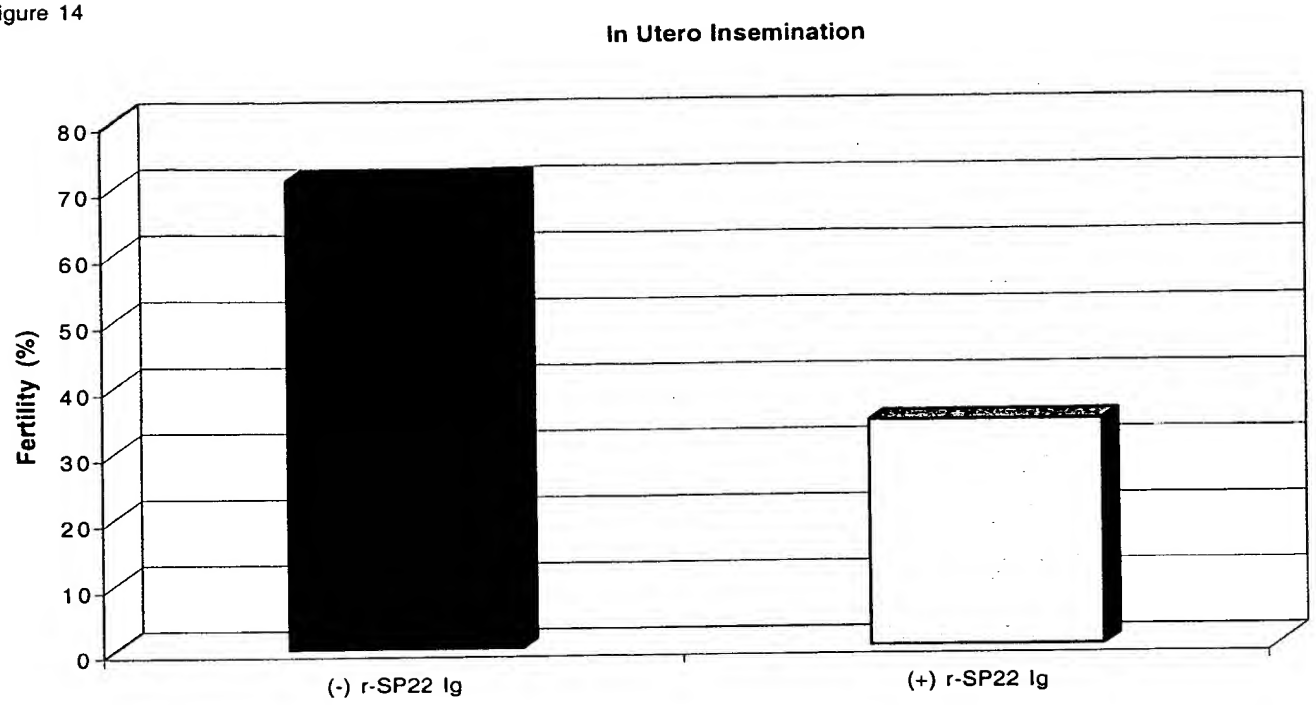

OD at 450 nm
0
0.5
1
1.5
2
2.5
3
3.5
Sequential Sp22 15 MER Peptides
MASKRALVILAKGAE
KRALVILAKGAEEME
LVILAKGAEEMETVI
LAKGAEEMETVIPVD
GAEEMETVIPVDIMR
EMETVIPVDIMRRAG
TVIPVDTMRRAGIKV
PVDIMRRAGIKVTVA
IMRRAGIKVTVAGLA
RAGIKVTVAGLAGKD
IKVTVAGLAGKDPVQ
TVAGLAGKDPVQCSR
GLAGKDPVQCSRDVV
GKDPVQCSRDVVICP
PVQCSRDVVICPDTS
CSRDVVICPDTSLEE
DVVICPDTSLEEAKT
ICPDTSLEEAKTQSP
DTSLEEAKTQGPYDV
LEEAKTQGPYDVVVL
AKTQGPYDVVVLPGG
QGPYDVVVLPGGNLG
YDVVVLPGGNLGAQN
VVLPGGNLGAQNLSE
PGGNLGAQNLSESAL
NLGAQNLSESALVKE
AQNLSESALVKEILK
LSESALVKEILKEQE
SALVKEILKEQENRK
VKEILKEQENRKGLI
ILKEQENRKGLIAAI
EQENRKGLIAAICAG
NRKGLIAAICAGPTA
GLIAAICAGPTALLA
AAICAGPTALLAHEV
CAGPTALLAHEVGFG
PTALLAHEVGFGCKV
LLAHEVGFGCKVTSH
HEVGFGCKVTSHPLA
GFGCKVTSHPLAKDK
CKVTSHPLAKDKMMN
TSHPLAKDKMMNGSH
PLAKDKMMNGSHYSY
KDKMMNGSHYSYSES
MMNGSHYSYSESRVE
GSHYSYSESRVEKDG
YSYSESRVEKDGLIL
SESRVEKDGLILTSR
RVEKDGLILTSRGPG
KDGLILTSRGPGTSF
LILTSRGPGTSFEFA
TSRGPGTSFEFALAI
GPGTSFEFALAIVEA
TSFEFALAIVEALSG
EFALAIVEALSGKDM
LAIVEALSGKDMANQ
VEALSGKDMANQVKA
LSGKDMANQVKAPLV
KDMANQVKAPLVLKD
Peptide C
LEEAKTQGPYDV
Peptide D
VKEILKEQENRKGLI
Peptide E
GFGCKVTSHPLAKDK

Figure 14


In Utero Insemination
Fertility (%)
80
70
60
50
40
30
20
10
0
(-) r-SP22 Ig
(+) r-SP22 Ig

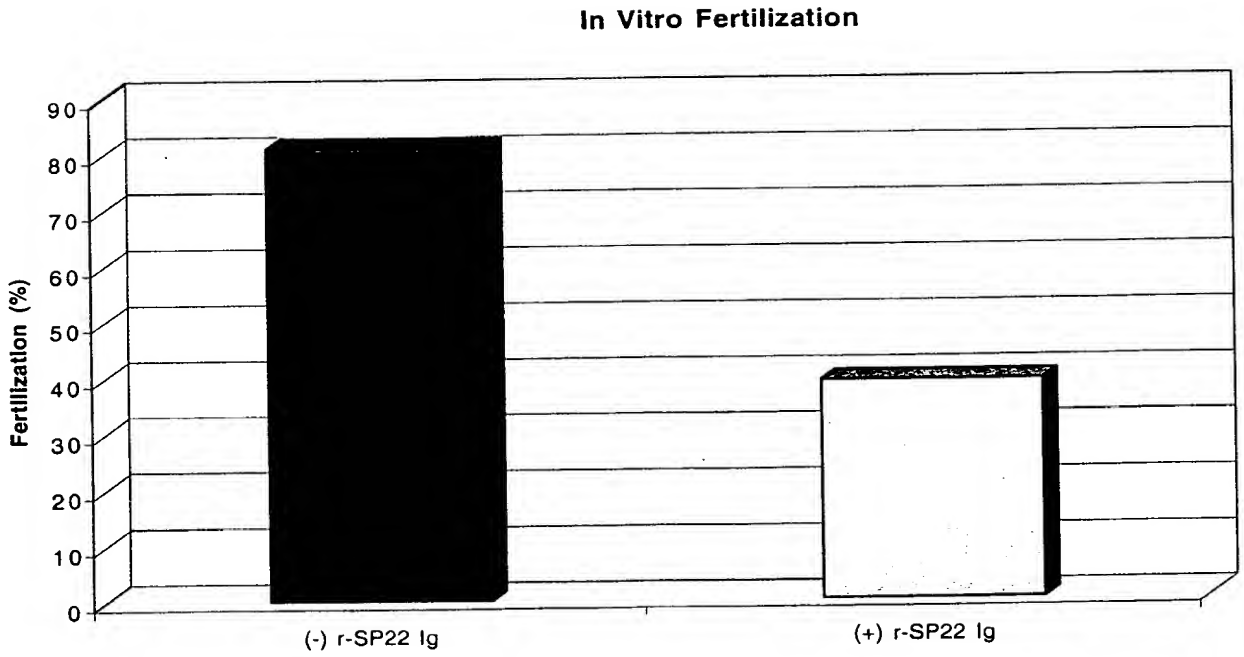

In Vitro Fertilization
Fertilization (%)
90
80
70
60
50
40
30
20
10
0
(-) r-SP22 Ig
(+) r-SP22 Ig

FIG. 15

```
1    xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxatggcatccaaaagagctctggtcatc 66
1    x x x x x x x x x x x x x M A S K R A L V I 22
67   ctagccaaaggagcagaggagatggagacagtgattcctgtggacatcatgcggcgagctgggatt 132
23   L A K G A E E M E T V I P V D I M R R A G I 44
133  aaagtcaccgttgcaggcttggctgggaaggaccccgtgcagtgtagccgtgatgtagtgatttgt 198
45   K V T V A G L A G K D P V Q C S R D V V I C 66
199  ccggataccagtctggaagaagcaaaaacacagggaccatacgatgtggttgttcttccaggagga 264
67   P D T S L E E A K T Q G P Y D V V V L P G G 88
265  aatctgggtgcacagaacttatctgagtcggctttggtgaaggagatcctcaaggagcaggagaac 330
89   N L G A Q N L S E S A L V K E I L K E Q E N 110
331  aggaagggcctcatagctgccatctgtgcgggtcctacggccctgctggctcacgaagtaggcttt 396
111  R K G L I A A I C A G P T A L L A H E V G F 132
397  ggatgcaaggttacatcgcacccattggctaaggacaaaatgatgaacggcagtcactacagctac 462
133  G C K V T S H P L A K D K M M N G S H Y S Y 154
463  tcagagagccgtgtggagaaggacggcctcatcctcaccagccgtgggcctgggaccagcttcgag 528
155  S E S R V E K D G L I L T S R G P G T S F E 176
528  tttgcgctggccattgtggaggcactcagtggcaaggacatggctaaccaagtgaaggccccgctt 594
177  F A L A I V E A L S G K D M A N Q V K A P L 198
595  gttctcaaagactagagagcccaagccctggaccctggacccccaggctgagcaggcattggaagc 660
199  V L K D *                                                          202
661  ccactagagagaccacagcccagtgaacctggcattggaagcccactagtgtgtccacagcccagt 726
727  gaacctcaggaactaacgtgtgaagtagcccgctgctcaggaatctcgccctggctctgtactatt 792
793  ctgagccttgctagtagaataaacagttccccaagctc                             830
```

FIGURE 16

SP22(A)

```
1       gctgtgcagagccgtctggcagggttgacctcctaaagggatattccatctttattaatcattag 65

66      tagtgtggtcagagacttagcaccattggtctcccccaacctggtccagacatttcagcagttta 130

131     tcggaacagcaacaacagcaacaaaaccttcaaaatttacaagtctttaagaaatagaaATGgca 195
1                                                                   M  A 2

196     tccaaaagagctctggtcatcctagccaaaggagcagaggagatggagacagtgattcctgtgga 260
3        S  K  R  A  L  V  I  L  A  K  G  A  E  E  M  E  T  V  I  P  V  D 24

261     catcatgcggcgagctgggattaaagtcaccgttgcaggcttggctgggaaggaccccgtgcagt 325
25       I  M  R  R  A  G  I  K  V  T  V  A  G  L  A  G  K  D  P  V  Q   45

326     gtagccgtgatgtagtgatttgtccggataccagtctggaagaagcaaaaacacagggaccatac 390
46       C  S  R  D  V  V  I  C  P  D  T  S  L  E  E  A  K  T  Q  G  P  Y  67

391     gatgtggttgttcttccaggaggaaatctgggtgcacagaacttatctgagtcggctttggtgaa 455
68       D  V  V  V  L  P  G  G  N  L  G  A  Q  N  L  S  E  S  A  L  V  K 89

456     ggagatcctcaaggagcaggagaacaggaagggcctcatagctgccatctgtgcgggtcctacgg 520
90       E  I  L  K  E  Q  E  N  R  K  G  L  I  A  A  I  C  A  G  P  T   110

521     ccctgctggctcacgaagtaggctttggatgcaaggttacatcgcacccattggctaaggacaaa 585
111      A  L  L  A  H  E  V  G  F  G  C  K  V  T  S  H  P  L  A  K  D  K 132

586     atgatgaacggcagtcactacagctactcagagagccgtgtggagaaggacggcctcatcctcac 650
133      M  M  N  G  S  H  Y  S  Y  S  E  S  R  V  E  K  D  G  L  I  L  T 154

651     cagccgtgggccttgggaccagcttcgagtttgcgctggccattgtggaggcactcagtggcaagg 715
155      S  R  G  P  G  T  S  F  E  F  A  L  A  I  V  E  A  L  S  G  K   175

716     acatggctaaccaagtgaaggccccgcttgttctcaaagacTAGagagcccaagccctggaccct 780
176      D  M  A  N  Q  V  K  A  P  L  V  L  K  D                       189

781     ggacccccaggctgagcaggcattggaagcccactagtgtgtccacagcccagtgaacctggcat 845

846     tggaagcccactagtgtgtccacagcccagtgaacctcaggaactaacgtgtgaagtagcccgct 910

911     gctcaggaatctcgccctggctctgtactattctgagccttgctagtagaataaacagttcccca 975
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